Amendments to the Claims

1. (Original) An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 2 and 4, and fragments thereof.

2. (Original) The isolated polypeptide of Claim 1, wherein the fragment comprises the amino acid residues 258 to 259 of SEQ ID NO: 2.

3. (Original) The isolated polypeptide of Claim 1, wherein the fragment comprises the amino acid residues 321 to 322 of SEQ ID NO: 4.

4. (Original) An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5 and 7, and fragments thereof.

5. (Original) The isolated nucleic acid of Claim 4, wherein the fragment comprises nucleotides 783 to 788 of SEQ ID NO: 1.

6. (Original) The isolated nucleic acid of Claim 4, wherein the fragment comprises nucleotides 972 to 977 of SEQ ID NO: 3.

7. (Original) The isolated nucleic acid of Claim 4, wherein the fragment comprises nucleotides 1186 to 1236 of SEQ ID NO: 5.

8. (Original) The isolated nucleic acid of Claim 4, wherein the fragment comprises nucleotides 1127 to 1176 of SEQ ID NO: 7.

9. (Original) An expression vector comprising the nucleic acid of Claim 4.

10. (Original) A host cell transformed with the expression vector of Claim 9.

11. (Currently Amended) A method for producing an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 2 and 4, and fragments thereof ~~the polypeptide of Claim 1~~, which comprises the steps of:

(1) culturing the host cell of Claim 10 under a condition suitable for the expression of the polypeptide; and

(2) recovering the polypeptide from the host cell culture.

12. (Original) An antibody specifically binding to the polypeptide of Claim 1.

13. (Currently Amended) A method for diagnosing the diseases associated with the deficiency of the SMAPK3 gene in a mammal, in particular cancers, which comprises detecting the nucleic acid of Claim 4 ~~or the polypeptide of Claim 1~~.

14. (Currently Amended) The method of Claim 13, wherein the detection of the nucleic acid ~~of Claim 4~~ comprises the steps of:

(1) extracting total RNA from a sample obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) to obtain a cDNA sample;

(3) bringing the cDNA sample into contact with the nucleic acid ~~of Claim 4~~; and

(4) detecting whether the cDNA hybridizes with the nucleic acid ~~of Claim 4~~.

15. (Original) The method of Claim 14 further comprising the step of determining the amount of hybridized sample.

16. (Currently Amended) The method of Claim 13, wherein the detection of the nucleic acid ~~of Claim 4~~ comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragment

comprising the nucleotides 783 to 788 of SEQ ID NO: 1, the nucleotides 972 to 977 of SEQ ID NO: 3, the nucleotides 1186 to 1236 of SEQ ID NO: 5, or the nucleotides 1127 to 1176 of SEQ ID NO: 7; and

(3) detecting whether the cDNA is obtained.

17. (Original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 783 to 788 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 788, or alternatively, the reverse primer has a sequence complementary to the nucleotides comprising the nucleotides 783 to 788 of SEQ ID NO: 1 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 783.

18. (Original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides 972 to 977 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 977, or alternatively, the reverse primer has a sequence complementary to the nucleotides comprising the nucleotides 972 to 977 of SEQ ID NO: 3 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 972.

19. (Original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides between 1186 to 1236 of SEQ ID NO: 5 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1236, or alternatively, the reverse primer has a sequence complementary to the nucleotides 1186 to 1236 of SEQ ID NO: 5 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 5

at any other locations upstream of nucleotide 1186.

20. (Original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides between 972 to 977 of SEQ ID NO: 7 and the reverse primer has a sequence complementary to the nucleotides comprising the nucleotide 1127 to 1176 of SEQ ID NO: 7.

21. (Original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 783 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 788.

22. (Original) The method of Claim 16, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 972 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 977.

23. (Original) The method of Claim 16, wherein the forward primer has a sequence the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 1186 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 1236.

24. (Original) The method of Claim 16, wherein the forward primer has a sequence the nucleotides of SEQ ID NO: 7 at any other locations upstream of nucleotide 972 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 7 at any other locations downstream of nucleotide 1176.

25. (Original) The method of Claim 21, the cDNA sample amplified from SEQ ID NO: 1 is 132bp shorter than that from SMAPK3.

26. (Original) The method of Claim 22, the cDNA sample amplified from

SEQ ID NO: 3 is 60bp shorter than that from SMAPK3.

27. (Original) The method of Claim 23, the cDNA sample amplified from SEQ ID NO: 5 is 51bp longer than that from SMAPK3.

28. (Original) The method of Claim 24, the cDNA sample amplified from SEQ ID NO: 7 is 9bp shorter than that from SMAPK3.

29. (Original) The method of Claim 16 further comprising the step of detecting the amount of the amplified cDNA sample.

30. (Cancel)

31. (Cancel)

32. (New) A method for diagnosing the diseases associated with the deficiency of the SMAPK3 gene in a mammal, in particular cancers, which comprises detecting the polypeptide of Claim 1.

33. (New) The method of Claim 32, wherein the detection of the polypeptide comprises the steps of contacting an antibody specifically binding to an isolated polypeptide comprising an amino acid sequence selected from the group of SEQ ID NOS: 2 and 4, and fragments thereof.

34. (New) The method of Claim 33 further comprising the step of determining the amount of the antibody-polypeptide complex.